

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:13:06 ; Search time 101.54 Seconds
(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089a-6
Perfect score: 293
Sequence: 1 LSLCTICSDFFDHSRDVAIAIHCCHTFHCLQCLIQWFTAPSRTPQCRIOV 51

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244	83.3	433	2 T30807	TRAF interacting p
2	127	43.3	310	2 C84701	hypothetical prote
3	125	42.7	325	2 F86321	F6A14.12 protein -
4	123	42.0	158	2 T13738	hypothetical prote
5	113	38.6	224	2 E86321	hypothetical prote
6	112	38.2	344	2 T05064	hypothetical prote
7	112	38.2	383	2 A86315	F2H15.19 protein -
8	110	37.5	274	2 T48296	hypothetical prote
9	108	36.9	489	2 T26069	hypothetical prote
10	107	36.5	137	2 T46904	hypothetical prote
11	107	36.5	551	2 S66695	probable membrane
12	106.5	36.3	506	2 F85016	probable RING zinc
13	106	36.2	367	2 H96764	protein RING zinc
14	106	36.2	425	2 T25457	hypothetical prote
15	106	36.2	524	2 F96572	protein F12M16.10
16	105	35.8	1238	2 T15919	hypothetical prote
17	104.5	35.7	441	2 F71425	hypothetical prote
18	104	35.5	351	2 F96597	hypothetical prote
19	102.5	35.0	237	2 G84678	probable RING zinc
20	102	34.8	180	2 T51859	probable RING zinc
21	102	34.8	292	2 T26684	hypothetical prote
22	101.5	34.6	425	2 A84849	probable RING zinc
23	100.5	34.3	157	2 T13027	RING-H2 finger pro
24	100.5	34.3	157	2 T51841	RING-H2 finger pro
25	99.5	34.0	206	2 C85067	hypothetical prote
26	99.5	34.0	1610	2 T11681	hypothetical prote
27	98.5	33.6	227	2 T00428	hypothetical prote
28	98	33.4	204	2 G84530	probable RING-H2 z
29	98	33.4	324	2 E84918	hypothetical prote

30	98	33.4	343	2 H96703	probable RING zinc
31	97.5	33.3	257	2 T48058	RING-H2 zinc finger
32	97	33.1	211	2 F86488	protein T32E20.33
33	97	33.1	235	2 T19328	hypothetical prote
34	97	33.1	407	2 G96835	hypothetical prote
35	96.5	32.9	194	2 C85130	probable RING zinc
36	96.5	32.9	203	2 T48129	hypothetical prote
37	96.5	32.9	304	2 T52079	hypothetical prote
38	96.5	32.9	408	2 T25524	probable RING zinc
39	96	32.8	145	2 B96705	hypothetical prote
40	96	32.8	377	2 T26958	unknown protein, 8
41	96	32.8	488	2 T10675	hypothetical prote
42	96	32.8	530	2 T50499	hypothetical prote
43	95.5	32.6	162	2 E84455	probable RING zinc
44	95	32.4	189	2 T05383	hypothetical prote
45	95	32.4	238	2 T49155	hypothetical prote

ALIGNMENTS

RESULT 1
T30807
TRAF interacting protein - Fugu rubripes
C:Species: Fugu rubripes
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T30807
R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrantia, Y.; Wheller, D.; Bishop, M.; Elgar, F.E.B. Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasmalogen related growth factors in the genome of A:Reference number: Z20880; MUID:99148833
A:Accession: T30807
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-433 <COT>
A:Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1
C:Genetics:
A:Gene: TRIP
A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match 83.3%; Score 244; DB 2; Length 433;
Best Local Similarity 83.0%; Pred. No. 2e-21;
Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTICSDFFDHSRDVAIHCCHTFHCLQCLIQWFTAPSRTPQCRIOV 50
|||||
Db 7 CTICSDFFDHSRDVAIHCCHTFHCLQCLIQWFTAPSRTPQCRIOV 53

RESULT 2
C84701
hypothetical protein At2g29840 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84701
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84701
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: GB:AE002093; NID:g3582320; PIDN:AAC35217.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29840
A:Map position: 2

Query Match 43.3%; Score 127; DB 2; Length 310;

Best Local Similarity 41.7%; Pred. No. 1,1e-07;
Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

Oy 3 LCITCSDFPDHSDVAIHCCHTFHLOCLIQWETAPSRPCPOCRIOY 50
Db 260 MCSICLDFPDGKRSIVLPCGHEFDDECAIKWFET--NHDCPLCRFKL 305

RESULT 3

F6A14.12 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: F86321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F86321

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1325 <STO>

A:Cross-references: GB:AE005172; NID:g6730707; PIDN:AAF27102.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 42.7%; Score 125; DB 2; Length 325;
Best Local Similarity 39.6%; Pred. No. 2e-07;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

Oy 3 LCITCSDFPDHSDVAIHCCHTFHLOCLIQWETAPSRPCPOCRIOY 50
Db 276 VCTICLDFPDGKRSIVLPCGHEFDDECAIKWF--VSHVCPCLCRLEL 321

RESULT 4

hypothetical protein 22E5.12 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13738

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL data library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17668

A:Accession: T13738

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <MUR>

A:Cross-references: EMBL:AL031765; NID:el371523; PID:el326038; PIDN:CAB41708.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:introns: 41/2

A:Note: EG:22E5.12

C:Superfamily: RING finger homology

F:4-54/Domain: RING finger homology <RRN>

Query Match 42.0%; Score 123; DB 2; Length 158;
Best Local Similarity 51.1%; Pred. No. 1,9e-07;
Matches 24; Conservative 4; Mismatches 17; Indels 2; Gaps 1;

Oy 3 LCITCSDFPDHSDVAIHCCHTFHLOCLIQWETAPSRPCPOCRIOY 49
Db 7 ICTICSEFRFTSDNIQSGHAFHEDCLDHW--RKOSRCPICRSQ 51

RESULT 5

hypothetical protein F6A14.13 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E86321

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1224 <STO>

A:Cross-references: GB:AE005172; NID:g6730708; PIDN:AAF27103.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 38.6%; Score 113; DB 2; Length 224;
Best Local Similarity 40.4%; Pred. No. 3,9e-06;
Matches 19; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

Oy 4 CTICSDFFPDHSDVAIHCCHTFHLOCLIQWETAPSRPCPOCRIOY 50
Db 175 CTICLDFPDGKRSIVLPCGHEFDDECAIKWFET--NHDCPLCRFKL 219

RESULT 6

hypothetical protein M3E9.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T05064

R:Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hohelsel, J.; Mewes, H.W.; Ma

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15396

A:Accession: T05064

A:Molecule type: DNA

A:Residues: 1-344 <BEV>

A:Cross-references: EMBL:AL022223

A:Experimental source: cultivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A:Note: M3E9.170

C:Superfamily: RING finger homology

F:225-275/Domain: RING finger homology <RRN>

Query Match 38.2%; Score 112; DB 2; Length 344;
Best Local Similarity 38.3%; Pred. No. 7,3e-06;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

Oy 4 CTICSDFFPDHSDVAIHCCHTFHLOCLIQWETAPSRPCPOCRIOY 50
Db 229 CSICLDFPDGKSEAKMPCKHKFHIRCTVPLELHSS--CPVCRYEL 273

RESULT 7

F2H15.19 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: A86315

R.Thellogiis, Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso
Chih, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hutzler, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: AB6315
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-583 <STO>
A:Cross-references: GB:AE005172; NID:99665074; PIDN:AAF97276.1; GSPDB:GN00141
A:Genetics:
A:Map position: 1

[illegible]

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RESULT      8
T48296
hypothetical protein F9G14.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T48296
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysheert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24491
A:Accession: T48296
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-274 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.60
C:Superfamily: RING finger homology
F:201-251/Domain: RING finger homology <RRN>

```

	Query Match Similarity	37.5%	Score 110;	DB: 2;	Length 274;
	Best Local Similarity	38.3%;	Pred. No.1e-05;		
	Matches 18;	Conservative 7;	Mismatches 20;	Indels 2;	Gaps 1;
OY	4 CTICSDFDHSRDVAAIHCGHTFHQCLIQWETAPASRTCPQCRIOV	50			
Db	205 CYICCEMSESGRDVCPCQCHFFHMCKLIPWL-SKKNKCPCCRFGL	249			

RESULT 9
T26069
hypothetical protein W02A11.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T26069
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20147
A:Accession: T26069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues:489 <ML>
A:Cross-references: EMBL:282062; PDB:1CAB; GSPDB:GN00019; CESP:W02A11.3
A:Experimental source: clone W02A11
A:Genetics:
A:Gene: CESP:W02A11.3
A:Map position: 1
A:Introns: 58/3, 129/3, 361/3, 444/3
C:Superfamily: RING_finger homology
F:429-479/Domain: RING_finger homology <RR>

	Query Match	Similarity	36.9%	Score	108	DB	2:	Length	489;	
	Best Local	Similarity	29.8%	Pred.	No	2.9e-05:				
	Matches	14:	Conservative	12;	Mismatches	19;	Indels	2;	Gaps	1;
Oy	4	CTICSDFDHSRDVAIHCGHTFHQCLLIQTWETAPSRTCPCORIOV	50							
		:	:	:	:	:	:			
Db	433	CTVCILSSFEDEGSIQKLRGNHVFHECCEIATKWLDI--NKKCPMCREII	477							

RESULT 10
T46904
hypothetical protein DKFZp761D081.1 - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C/Accession: T46904
R/Ottensaeider, B.; Obermaier, B.; Mewes, H.W.; Well, B.; Wiemann, S.
submitted to the Protein Sequence Database, February 2000
A/Reference number: Z24136

A:Accession: T46904
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <AA>
A:Cross-references: EMBL:AL157474
A:Experimental source: adult amygdala; clone DKFZp761D081
C:Genetics:
A:Note: DKFZp761D081.1
C:Superfamily: RING finger homology
F:81-131/Domain: RING finger homology <RNN>

Query Match	36.5%	Score 107	DB 2	Length 137
Best Local Similarity	38.3%	Pred. No. 1.3e-05		
Matches 18	Conservative 7	Mismatches 20	Indels 2	Gaps 1
QY	4	CTCSCDFDHSRDVAAIHCGHTFHLQCLIQWETAFSRPCPOCRIV	50	
Db	85	CTCISILIEEGEDVRLPCMLFHOVCYQWMLT--NKKCPICRIV	129	

RESULT 11
566695
probable membrane protein Y0L013C - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein O241
C:Species: *Saccharomyces cerevisiae*
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Sep-2000
C:Accession: S66695
R:Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996

A:Molecule type: DNA
A:Residues: 1-551 <HUG>
A:Cross-references: EMBL:Z74755, NID:91419784, PID:e252259, PID:91419785, MIPS:YOL013
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:HRD1
A:Cross-references: SGD:S0005373, MIPS:YOL013C
A:Map position: 15L
C:Superfamily: RING finger homology
C:Keywords: Transmembrane protein
F:10-26/Domain: transmembrane #status predicted <TM1>
F:46-62/Domain: transmembrane #status predicted <TM2>

Db 472 CTICQSFKNEXIALTLDCGHEYHAECLERKML--IVKNVCPICK 513

RESULT 16

hypotheical protein EEBD8.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000

C:Accession: T15919

R:Chisoe, S.

Submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid EEBD8.

A:Reference number: 218428

A:Accession: T15919

A:Status: preliminary; translated from GB/EMBL/DDbf

A:Molecule type: DNA

A:Residues: 11238 <CHT>

A:Cross-references: EMBL:U23484; NID:g733597; PID:g733606; PIDN:MAC46769.1; CESP:EEBD8.9

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:EEBD8.9

A:Introns: 16/3; 60/3; 140/1; 192/3; 269/2; 402/2; 637/3; 717/3; 769/1; 855/3; 888/3; 10

C:Superfamily: RING finger homology

F:904-950/Domain: RING finger homology <RRN>

Query Match 35.8%; Score 105; DB 2; Length 1238;

Best Local Similarity 44.7%; Pred. No. 0.00015;

Matches 21; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

Qy 1 LSLCTICSDFFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCPCOR 47

Db 905 LPTCAVCLERMDSD-VLAILCNHSPHARCLEQWAD----NTCVCYCR 945

RESULT 17

F71425

hypotheical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

A:Variety: Columbia

C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000

C:Accession: F71425

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk

P.; Medler, H.; Medler, S.; Kottler, P.; Entian, K.D.; Rieger, M.; Scheffter, M.; Funk, B.

Nature 391, 485-486, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans

C.; Chalwatzi, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A:Reference number: A71400; MUID:98121113

A:Accession: F71425

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-441 <BEV>

A:Cross-references: GB:297340; NID:g2244950; PID:e326963; PID:g2244955

C:Genetics:

A:Map position: 4COP9-463845

C:Superfamily: RING finger homology

F:278-329/Domain: RING finger homology <RRN>

Query Match 35.7%; Score 104.5; DB 2; Length 441;

Best Local Similarity 39.6%; Pred. No. 7e-05;

Matches 19; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

Qy 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCPCOR 50

Db 282 CSQLSEFKDNESGRVMPNCKHTFHVHCIDMWFHSHS--CPICRSQ 327

RESULT 18

F96597

hypotheical protein TSA14.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96597

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.P.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F96597

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-351 <STO>

A:Cross-references: GB:AE005173; NID:g4204263; PIDN:AAD10644.1; GSPDB:GN00141

C:Genetics:

A:Gene: TSA14.7

A:Map position: 1

Query Match 35.5%; Score 104; DB 2; Length 351;

Best Local Similarity 38.3%; Pred. No. 6.6e-05;

Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCPCOR 50

Db 223 CSQLDFEIGTEAKMPCTHKFHSDDLPMLEHSS--CPVCRYQL 267

RESULT 19

G84678

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: G84678

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: G84678

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <STO>

A:Cross-references: GB:AE002093; NID:g4510422; PIDN:AAD21508.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g27940

A:Map position: 2

Query Match 35.0%; Score 102.5; DB 2; Length 237;

Best Local Similarity 42.2%; Pred. No. 7.1e-05;

Matches 19; Conservative 4; Mismatches 19; Indels 3; Gaps 2;

Qy 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCPCOR 47

Db 140 CVCILDFEIGEYKVIPLHGHVHVCDVTLWLSYV--TCPICR 182

RESULT 20

T51859

RING-H2 finger protein RHG1a [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51859

R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.

FEBS Lett. 436, 283-7, 1998


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A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488
A:Accession: CB5067
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STO>
C:Cross-references: GB:NC_001268; NID:g7267295; PIDN:CAB81077.1; GSPDB:GN00140
C:Genetics:
A:Gene position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING FA
Oy      4 CTICSDFF--DHSRDVAIHGHHFHCLOCLIQWETAPSRPCQRIQV 50
Db      157 CILCESLVSGPKRPDYRTMCSHVFHNGCLEMLKR--KNTCPICKREI 204

RESULT 26
T11681
hypothetical protein SPBC21D10.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T11681
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z17313
A:Accession: T11681
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-1610 <SEE>
C:Cross-references: EMBL:AL031536; NID:e1319499; PID:e1319508
A:Experimental source: strain 972h(-)
C:Genetics:
A:Map position: IIR
A:introns: 10/2
A>Note: SPBC21D10.09c
C:Superfamily: RING finger homology
P:1554-1609/Domain: RING finger homology <RR>

Query Match          34.0%; Score 99.5; DB 2; Length 1610;
Best Local Similarity 38.3%; Pred. No. 0.00082;
Matches 18; Conservative 5; Mismatches 21; Indels 3; Gaps 1;

Oy      4 CTICSDFFDHSRDVAIHCG--HTFHQLCIQWETAPSRTPCPCR 47
        |||         :   || | || | :||:: | || |
Db      1558 CAICYSVLSEVERTLPNKRCGTCRHKFHASCLYKMFKSSNSSCPICR 1604

RESULT 27
T00428
hypothetical protein At2g47560 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T30B22.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00428; G84916
R:Rounsley, S.D.; Lin, X.; Ketchem, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masera
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.
A:Reference number: Z14149
A:Accession: T00428
A>Status: translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-227 <ROU>
C:Cross-references: EMBL:AC002535; NID:g2529657; PID:g2529671
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

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euss.D.; Nielsen, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: E84916
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-227 <STO>
A:Cross-references: GB:E002093; NID:g2529671; PIDN:AAC62854.1; GSPDB:GN00139
C:Genetics:
A:Gene: T3OB22.14; AC2g47560
A:Map position: 2
C:Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology
F:104-155/Domain: RING finger homology <RNF>

RESULT 28
Query Match 33.6%; Score 98.5; DB 2; Length 227;
Best Local Similarity 37.5%; Pred. No. 0.0002;
Matches 18; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

QY 4 CTCGDFDHSRDVAIHCGHTFHLOCLIQMFPETAPSRTPQCRIQV 50
      |||::||::||::||::||::||::||::||::||::||::||
Db 108 CSVCSFEFEDEGRLLPKCGSHFHDICDIWFNRS--RSTCPPLCRAPV 153

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: E84918
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-224 <STO>
A:Cross-references: GB:AE002093; NID:g3738284; PIDN:AAC63626.1; GSPDB:GN00139
A:Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 204;
Best Local Similarity 36.2%; Pred. No. 0.00021;
Matches 17; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

QY 4 CTTCGDFDHSRDVAIHCGHTFHLOCLIQMFPETAPSRTPQCRIQV 50
      |||::||::||::||::||::||::||::||::||::||::||
Db 158 CATCDREKKKGETLVHPCAKHFHSICLIPMLDT--NWYCPIKRIDI 202

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
hypothetical protein At2g47700 [imported] - Arabidopsis thaliana
C:Species: Arabidops thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84918
R:Lili, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: E84918
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-224 <STO>
A:Cross-references: GB:AE002093; NID:g3738284; PIDN:AAC63626.1; GSPDB:GN00139
A:Map position: 2
```

C:Genetics:
A:Gene: At2g47700
A:Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 324;
Best Local Similarity 41.3%; Pred. No. 0.00032;
Matches 19; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTIC--SDFPDHSDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 47
Db 38 CSICLESYLDGTRSKATLQCGHFDICISAFNMKGAMCPCNR 83

RESULT 30
H96703
probable RING zinc finger protein T23K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96703
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96703
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <STO>
A:Cross-references: GB:AE005173; NID:96553889; PIDN:AAF16555.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23K23.8
A:Map position: 1

Query Match 33.4%; Score 98; DB 2; Length 343;
Best Local Similarity 27.7%; Pred. No. 0.00033;
Matches 13; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 50
Db 292 CCICLSTEDGAEVLSPCHHHSCTVKKLM--NATCPLCKFNI 336

RESULT 31
T48058
RING-H2 zinc finger protein ARL5 - Arabidopsis thaliana
N:Alternate names: protein F26K9.120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C:Accession: T48058
R:Bioecker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetler, F.; Salanoubat
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24465
A:Accession: T48058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <BLO>
A:Cross-references: EMBL:AL162651
A:Experimental source: cultivar Columbia; BAC clone F26K9
C:Genetics:
A:Map position: 3
A:Note: F26K9.120
C:Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology
F;109-160/Domain: RING finger homology <RRN>

Query Match 33.3%; Score 97.5; DB 2; Length 257;
Best Local Similarity 37.3%; Pred. No. 0.0003;
Matches 19; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

OY 1 LSLCTIC--SDFPDHSDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 50
Db 110 LECCSVCLSEFEDEDEGRVLPKCGHVFHDCIDYFRSRSS--CPLCRAPV 158

RESULT 32
F86488
protein T32E20.33 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86488
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <STO>
A:Cross-references: GB:AE005172; NID:98778785; PIDN:AAF79793.1; GSPDB:GN00141
C:Genetics:
A:Gene: T32E20.33
A:Map position: 1

Query Match 33.1%; Score 97; DB 2; Length 211;
Best Local Similarity 35.6%; Pred. No. 0.00029;
Matches 16; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

OY 3 LCTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 47
Db 85 ICCICODRFORACVGRKLCNGHNFHINSVKPWLIT--KKOCPCVQ 127

RESULT 33
T19328
hypothetical protein Cl6C10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T19328
R:Lloyd, C.
submitted to the EMBL data library, November 1994
A:Reference number: Z19108
A:Accession: T19328
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <NTL>
A:Cross-references: EMBL:Z46787; PIDN:CAA86745.1; GSPDB:GN00021; CESP:Cl6C10.7
A:Experimental source: clone Cl6C10
C:Genetics:
A:Gene: CESP:Cl6C10.7
A:Map position: 3
A:Insertions: 23/2; 105/3; 196/1
C:Superfamily: RING finger homology
F;22-72/Domain: RING finger homology <RRN>

Query Match 33.1%; Score 97; DB 2; Length 235;
Best Local Similarity 40.0%; Pred. No. 0.00032;
Matches 18; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

OY 4 CTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAP--SRPCPCR 47

Db 26 CNIC---LDAAKDAVSLGHLFCMPCLSQMLDIFRPNNGVCPEVK 67

RESULT 34
96835
Probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96835
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Mailli, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96835
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <SMD>
C:Genetics:
A:Cross-references: GB:AEO05173; NID:g6751714; PIDN:AAF27696.1; GSPDB:GN00141
A:Gene: F516.15
A:Map position: 1

Query Match 33.1% Score 97; DB 2; Length 407;
Best Local Similarity 33.3%; Pred. No. 0.0005;
Matches 16; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Oy 4 CTTCGDFHSDVAIHGHGFHFLOCLIQMFETAPSRCTGCGRIOVG 51
||| | | | | | | | | | | | | | | | | | | | |
Db 355 CCCTCTRGDEQVRELPCSHVFHVDCYDKWLKT--NAIPLCKNEVG 400

RESULT 35
CB5130
hypothetical protein AT4g12190 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: CB5130
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: CB5130
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-194 <SMD>
C:Genetics:
A:Cross-references: GB:NC_001268; NID:g7267920; PIDN:CAB78262.1; GSPDB:GN00140
A:Gene: AT4g12190
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein Fl6J13.210; RING f

Query Match 32.9% Score 96.5; DB 2; Length 194;
Best Local Similarity 34.0%; Pred. No. 0.00031;
Matches 17; Conservative 9; Mismatches 19; Indels 5; Gaps 2;

Oy 4 CTTCGDF---DHSNDVAIHGHGFHFLOCLIQMFETAPSRCTGCGRIOVG 50
||| | | | | | | | | | | | | | | | | | | | |
Db 145 CSICLESVSGPKPRDITRMTCSHVFHNGCLEWLR--KNTPCLPRTLE 192

RESULT 36
T48129
hypothetical protein T4c9.30 - Arabidopsis thaliana

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C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C:Accession: T48129
R:Beyan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z24485
A:Accession: T48129
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <BEV>
A:Cross-references: EMBL:AL080318
A:Experimental source: cultivar Columbia; BAC clone T4C9
C:Genetics:
A:Map position: 4
A:Introns: 9/3
A>Note: T4C9.30
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING
F.150-203/Domains: RING finger homology <RRN>

Query Match          32.9%; Score 96.5; DB 2; Length 203;
Best Local Similarity 34.0%; Pred. No. 0.00032;
Matches 17; Conservative 9; Mismatches 19; Indels 5; Gaps 2;

OY      4 CTICDFF---DHSRDVAIHCGHTFHLOCLIQMFETAPSTCCQCRQV 50
       1111 :         11 : 11111111 :         11111 :
Db     154 CSCIESTLVSGKPRDIRMTCSHVFHNGCLLEWLKR--KNTCPICRETL 201

RESULT 37
T52079
probable zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52079
R:Martinezgarcia, M.; GarciduenaSpina, C.; Guzman, P.
Mol. Gen. Genet. 252, 587-596, 1996
A>Title: Gene isolation in arabidopsis-thaliana by conditional overexpression of cdna
A:Reference number: Z04056
A:Accession: T52079
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-304 <MAR>
A:Cross-references: EMBL:L76926; PID:NACG7829.1

Query Match          32.9%; Score 96.5; DB 2; Length 304;
Best Local Similarity 37.8%; Pred. No. 0.00045;
Matches 17; Conservative 7; Mismatches 18; Indels 3; Gaps 2;

OY      4 CTCSDPFDSHRDVAAI-HCGHTFHLOCLIQMFETAPSTPCPCR 47
       11111111 : : 11111111 : : 11111111 : : 11111111 :
Db     119 CAVCLSEFEESRTGRVLPCNQHTFHVDICIDIMFHS--HSTCPCLR 161

RESULT 38
T25524
hypothetical protein C06A5.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25524
R:Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A>Description: The sequence of C. elegans cosmid C06A5.
A:Reference number: Z20044
A:Accession: T25524
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-408 <DAV>
A:Cross-references: EMBL:U97193; PID:NAB52442.1; GSPDB:GN00019; CESP:C06A5.9
A:Experimental source: strain Bristol N2; clone C06A5
C:Genetics:
A:Gene: CESP:C06A5.9

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